



PCT

RAW SEQUENCE LISTING

DATE: 07/16/2004

PATENT APPLICATION: US/10/501,039

TIME: 10:14:15

Input Set : A:\Sequence Listing PCT-JP03-00117.txt

Output Set: N:\CRF4\07162004\J501039.raw

3 <110> APPLICANT: Tetsuro Kokubo, Masahiro Shirakawa, and Jeremy Robin Howard Tame
 5 <120> TITLE OF INVENTION: Method of monitoring gene expression
 7 <130> FILE REFERENCE: 4439-4023
 C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/501,039
 C--> 10 <141> CURRENT FILING DATE: 2004-07-08
 12 <150> PRIOR APPLICATION NUMBER: JP P2002-002396
 13 <151> PRIOR FILING DATE: 2002-01-09
 15 <160> NUMBER OF SEQ ID NOS: 14
 17 <170> SOFTWARE: PatentIn Ver. 2.1
 19 <210> SEQ ID NO: 1
 20 <211> LENGTH: 2487
 21 <212> TYPE: DNA
 22 <213> ORGANISM: *Saccharomyces cerevisiae*
 24 <220> FEATURE:
 25 <221> NAME/KEY: CDS
 26 <222> LOCATION: (1)..(2484)
 28 <400> SEQUENCE: 1

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30	Met	Leu	Phe	Gly	Val	Lys	Leu	Ala	Asn	Glu	Val	Tyr	Pro	Pro	Trp	Lys	
31	1			5				10					15				
33	ggt	tct	tat	att	aat	tat	gag	ggc	ttg	aaa	aaa	ttc	ctg	aag	gaa	gat	96
34	Gly	Ser	Tyr	Ile	Asn	Tyr	Glu	Gly	Leu	Lys	Lys	Phe	Leu	Lys	Glu	Asp	
35			20				25					30					
37	agc	gtg	aag	gat	gga	agt	aac	gat	aag	aaa	gca	cgc	tgg	gac	gat	tca	144
38	Ser	Val	Lys	Asp	Gly	Ser	Asn	Asp	Lys	Lys	Ala	Arg	Trp	Asp	Asp	Ser	
39			35				40				45						
41	gat	gaa	tcc	aag	ttt	gtg	gaa	gag	ttg	gat	aag	gaa	ctt	gaa	aaa	gtc	192
42	Asp	Glu	Ser	Lys	Phe	Val	Glu	Leu	Asp	Lys	Glu	Leu	Glu	Lys	Val		
43		50				55					60						
45	tat	ggt	ttt	caa	cta	aaa	aag	tac	aat	aac	ttg	atg	gag	aga	ttg	tcc	240
46	Tyr	Gly	Phe	Gln	Leu	Lys	Lys	Tyr	Asn	Asn	Leu	Met	Glu	Arg	Leu	Ser	
47	65				70			75				80					
49	cat	ctg	gag	aaa	caa	aca	gat	acg	gaa	gca	gcc	ata	aag	gcc	ttg	gac	288
50	His	Leu	Glu	Lys	Gln	Thr	Asp	Thr	Glu	Ala	Ala	Ile	Lys	Ala	Leu	Asp	
51				85			90				95						
53	gct	gat	gca	ttc	caa	cgt	gta	ttg	gag	gaa	ctg	tta	agc	gag	tct	acc	336
54	Ala	Asp	Ala	Phe	Gln	Arg	Val	Leu	Glu	Glu	Leu	Leu	Ser	Glu	Ser	Thr	
55			100				105				110						
57	gaa	tta	gac	aat	ttt	aag	aga	ttg	aac	ttt	act	ggg	ttt	gct	aag	att	384
58	Glu	Leu	Asp	Asn	Phe	Lys	Arg	Leu	Asn	Phe	Thr	Gly	Phe	Ala	Lys	Ile	
59			115				120				125						
61	gtt	aag	aaa	cat	gac	aag	cta	tat	cca	aag	tat	cca	tct	gtt	aaa	tct	432
62	Val	Lys	Lys	His	Asp	Lys	Leu	Tyr	Pro	Lys	Tyr	Pro	Ser	Val	Lys	Ser	



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63	130	135	140	
65	ttg ttg gaa gtt aga tta aag gaa ttg cct tcc cat tcg gaa gaa tat	480		
66	Leu Leu Glu Val Arg Leu Lys Glu Leu Pro Ser His Ser Glu Glu Tyr			
67	145	150	155	160
69	tcc cca ttg ttg tat cgt att tca ttt ttg tac aac att ttg aga agt	528		
70	Ser Pro Leu Leu Tyr Arg Ile Ser Phe Leu Tyr Asn Ile Leu Arg Ser			
71		165	170	175
73	aat ttt aac act gca tct gaa ccc tta gcc agc gct tct aag ttt tct	576		
74	Asn Phe Asn Thr Ala Ser Glu Pro Leu Ala Ser Ala Ser Lys Phe Ser			
75		180	185	190
77	agc att gtc agc aat gac ata gac atg aat ttc aga agc ttt aaa ttt	624		
78	Ser Ile Val Ser Asn Asp Ile Asp Met Asn Phe Arg Ser Phe Lys Phe			
79		195	200	205
81	tgg gtt cat aat gac aac tta atg gag gtc aaa aca aga atc ttg aga	672		
82	Trp Val His Asn Asp Asn Leu Met Glu Val Lys Thr Arg Ile Leu Arg			
83		210	215	220
85	cat ctt ccc gtg ttg gtc tac gcc aat gtt ccc tcc gaa aac gat gac	720		
86	His Leu Pro Val Leu Val Tyr Ala Asn Val Pro Ser Glu Asn Asp Asp			
87	225	230	235	240
89	ctg gtc aat aga ttc gaa tca gat ata tca aat aat gat gaa att gtg	768		
90	Leu Val Asn Arg Phe Glu Ser Asp Ile Ser Asn Asn Asp Glu Ile Val			
91		245	250	255
93	ggt agt tcg agc tcc act agt agc gta gaa cat ggc ttg gga gcg cgc	816		
94	Gly Ser Ser Ser Ser Thr Ser Ser Val Glu His Gly Leu Gly Ala Arg			
95		260	265	270
97	tcc ttc gat cca tta atc aac acg cta tat ttt gac aat gag cat ttt	864		
98	Ser Phe Asp Pro Leu Ile Asn Thr Leu Tyr Phe Asp Asn Glu His Phe			
99		275	280	285
101	gaa tta tat aac gac aag tta tta aag tta aat tca gca cct act tta	912		
102	Glu Leu Tyr Asn Asp Lys Leu Leu Lys Leu Asn Ser Ala Pro Thr Leu			
103		290	295	300
105	aga tta agg tgg act ggc cag tta tct gat aag ccg gat att ttc ttg	960		
106	Arg Leu Arg Trp Thr Gly Gln Leu Ser Asp Lys Pro Asp Ile Phe Leu			
107	305	310	315	320
109	gaa aag aaa act ctt att gaa gac gaa gcc act ggg aag tct gaa ttt	1008		
110	Glu Lys Lys Thr Leu Ile Glu Asp Glu Ala Thr Gly Lys Ser Glu Phe			
111		325	330	335
113	gat cta act aaa ttg caa ttg aaa caa aaa ttc att aac ggg ttt att	1056		
114	Asp Leu Thr Lys Leu Gln Leu Lys Gln Lys Phe Ile Asn Gly Phe Ile			
115		340	345	350
117	ttc gaa ggt gat aag aaa ttt aaa gaa caa act ttg aaa aag tta aaa	1104		
118	Phe Glu Gly Asp Lys Lys Phe Lys Glu Gln Thr Leu Lys Lys Leu Lys			
119		355	360	365
121	gaa agt ggt acg gca ggg aga gac ctg gaa agg tta gaa gaa gat ttc	1152		
122	Glu Ser Gly Thr Ala Gly Arg Asp Leu Glu Arg Leu Glu Glu Asp Phe			
123		370	375	380
125	tct gag att caa aac ttt att atc aag aat gaa ttg caa cca gtt ttt	1200		
126	Ser Glu Ile Gln Asn Phe Ile Ile Lys Asn Glu Leu Gln Pro Val Phe			
127	385	390	395	400

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129	aga	act	gtt	tac	acc	aga	act	gct	ttc	cag	att	ccc	ggc	gat	gac	aag	1248
130	Arg	Thr	Val	Tyr	Thr	Arg	Thr	Ala	Phe	Gln	Ile	Pro	Gly	Asp	Asp	Lys	
131					405					410						415	
133	ata	aga	gta	acc	att	gac	tct	aat	att	gta	ttc	atc	aag	gag	gat	tca	1296
134	Ile	Arg	Val	Thr	Ile	Asp	Ser	Asn	Ile	Val	Phe	Ile	Lys	Glu	Asp	Ser	
135					420					425						430	
137	ttc	gac	aga	gag	cgt	cca	att	aga	gac	cct	aat	acc	tgg	cat	aga	act	1344
138	Phe	Asp	Arg	Glu	Arg	Pro	Ile	Arg	Asp	Pro	Asn	Thr	Trp	His	Arg	Thr	
139					435					440						445	
141	gat	att	gat	gcc	aat	gtt	gca	aat	ccc	ttg	aaa	ttc	ctg	aga	gga	ggc	1392
142	Asp	Ile	Asp	Ala	Asn	Val	Ala	Asn	Pro	Leu	Lys	Phe	Leu	Arg	Gly	Gly	
143					450					455						460	
145	gag	tat	gct	aag	ttt	cct	tat	tca	gta	atg	gaa	att	aaa	gtg	aaa	agt	1440
146	Glu	Tyr	Ala	Lys	Phe	Pro	Tyr	Ser	Val	Met	Glu	Ile	Lys	Val	Lys	Ser	
147	465					470					475					480	
149	tca	tta	gat	tct	tcg	atg	tct	gcc	agt	tct	atg	att	tct	aat	gta	aaa	1488
150	Ser	Leu	Asp	Ser	Ser	Met	Ser	Ala	Ser	Ser	Met	Ile	Ser	Asn	Val	Lys	
151					485						490					495	
153	ctg	cct	aaa	aag	cat	ggt	caa	tgg	ctg	aac	gat	ttg	aca	aat	tct	cat	1536
154	Leu	Pro	Lys	Lys	His	Gly	Gln	Trp	Leu	Asn	Asp	Leu	Thr	Asn	Ser	His	
155					500					505						510	
157	ttg	gtc	aaa	gaa	att	cca	aag	ttt	tct	atc	ttt	gtg	caa	ggt	gtg	gca	1584
158	Leu	Val	Lys	Glu	Ile	Pro	Lys	Phe	Ser	Ile	Phe	Val	Gln	Gly	Val	Ala	
159					515						520					525	
161	tca	ttg	tat	gga	gat	gat	gaa	aaa	tta	gat	atc	tta	cca	ttt	tgg	tta	1632
162	Ser	Leu	Tyr	Gly	Asp	Asp	Glu	Lys	Leu	Asp	Ile	Leu	Pro	Phe	Trp	Leu	
163					530						535					540	
165	cca	gat	ttg	gaa	aca	gat	att	aga	cag	gat	cct	aag	caa	gca	tat	gag	1680
166	Pro	Asp	Leu	Glu	Thr	Asp	Ile	Arg	Gln	Asp	Pro	Lys	Gln	Ala	Tyr	Glu	
167	545					550					555					560	
169	gag	gaa	aag	aaa	aaa	ctg	ttg	aaa	caa	aaa	gag	ata	caa	aag	aaa	att	1728
170	Glu	Glu	Lys	Lys	Lys	Leu	Leu	Lys	Gln	Lys	Glu	Ile	Gln	Lys	Lys	Ile	
171					565						570					575	
173	gat	gga	atg	aga	agg	ctt	tcc	aac	tta	aaa	gag	cct	caa	cat	caa	gca	1776
174	Asp	Gly	Met	Arg	Arg	Leu	Ser	Asn	Leu	Lys	Glu	Pro	Gln	His	Gln	Ala	
175					580						585					590	
177	gca	gta	ccg	gta	tct	caa	gag	gaa	aat	gag	cgt	att	acc	tct	caa	ggt	1824
178	Ala	Val	Pro	Val	Ser	Gln	Glu	Glu	Asn	Glu	Arg	Ile	Thr	Ser	Gln	Gly	
179					595						600					605	
181	gat	ttg	gag	gca	gac	ggt	tca	tcc	gat	gag	gaa	act	gag	caa	gaa	cct	1872
182	Asp	Leu	Glu	Ala	Asp	Gly	Ser	Ser	Asp	Glu	Glu	Thr	Glu	Gln	Glu	Pro	
183					610						615					620	
185	cat	tcg	aaa	aga	tca	aag	aaa	gtt	cgg	aga	aga	aaa	ccc	aag	gcc	act	1920
186	His	Ser	Lys	Arg	Ser	Lys	Lys	Val	Arg	Arg	Arg	Lys	Pro	Lys	Ala	Thr	
187	625					630					635					640	
189	ttc	ttg	aga	att	ttg	gcc	ggt	aga	gat	cca	aag	tta	atg	ggg	gtg	gat	1968
190	Phe	Leu	Arg	Ile	Leu	Ala	Gly	Arg	Asp	Pro	Lys	Leu	Met	Gly	Val	Asp	
191					645						650					655	
193	tct	gaa	gaa	gaa	gaa	att	gaa	ttg	cca	cct	ggt	gtg	aaa	aaa	cca	tta	2016

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197 aat ttg tta aaa aat gct ggt cct gta aac gtg gag gca aag gtt tgg 2064
198 Asn Leu Leu Lys Asn Ala Gly Pro Val Asn Val Glu Ala Lys Val Trp
199          675          680          685
201 ctt gcc aac gaa cgt aca ttt aac aga tgg tta agt gtc acc agt tta 2112
202 Leu Ala Asn Glu Arg Thr Phe Asn Arg Trp Leu Ser Val Thr Ser Leu
203          690          695          700
205 ttg agt gtt ttg acg ttc tca att tat aat tct gtg aag aaa gcc gaa 2160
206 Leu Ser Val Leu Thr Phe Ser Ile Tyr Asn Ser Val Lys Lys Ala Glu
207 705          710          715          720
209 tac ccc act ttg gct aac tac atg gca tac gta tat ttt ggt cta acg 2208
210 Tyr Pro Thr Leu Ala Asn Tyr Met Ala Tyr Val Tyr Phe Gly Leu Thr
211          725          730          735
213 ata ttc tgt gct tta tgg tcc tat tcc att tat atg aaa aga gtt gat 2256
214 Ile Phe Cys Ala Leu Trp Ser Tyr Ser Ile Tyr Met Lys Arg Val Asp
215          740          745          750
217 att att caa caa aga agc ggt caa cat cta gat gca cca ctt ggt cca 2304
218 Ile Ile Gln Gln Arg Ser Gly Gln His Leu Asp Ala Pro Leu Gly Pro
219          755          760          765
221 gtt ttg gtt tct ata gtt tta ttt gtc act tta gtg gtt aat ttt gtt 2352
222 Val Leu Val Ser Ile Val Leu Phe Val Thr Leu Val Val Asn Phe Val
223          770          775          780
225 atg gcg ttt aga aat gca gca aag tct cgt caa gag ttg caa ata cag 2400
226 Met Ala Phe Arg Asn Ala Ala Lys Ser Arg Gln Glu Leu Gln Ile Gln
227 785          790          795          800
229 aat tta gaa gtt cct gaa aga ata cca gaa gta tta agg cca ctt caa 2448
230 Asn Leu Glu Val Pro Glu Arg Ile Pro Glu Val Leu Arg Pro Leu Gln
231          805          810          815
233 aat tat cta ttc aag tta atg ggg cca agc agt gat tag 2487
234 Asn Tyr Leu Phe Lys Leu Met Gly Pro Ser Ser Asp
235          820          825
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239 <211> LENGTH: 828
240 <212> TYPE: PRT
241 <213> ORGANISM: Saccharomyces cerevisiae
243 <400> SEQUENCE: 2
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248          20          25          30
250 Ser Val Lys Asp Gly Ser Asn Asp Lys Lys Ala Arg Trp Asp Asp Ser
251          35          40          45
253 Asp Glu Ser Lys Phe Val Glu Glu Leu Asp Lys Glu Leu Glu Lys Val
254          50          55          60
256 Tyr Gly Phe Gln Leu Lys Lys Tyr Asn Asn Leu Met Glu Arg Leu Ser
257 65          70          75          80
259 His Leu Glu Lys Gln Thr Asp Thr Glu Ala Ala Ile Lys Ala Leu Asp
260          85          90          95

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262 Ala Asp Ala Phe Gln Arg Val Leu Glu Glu Leu Leu Ser Glu Ser Thr
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265 Glu Leu Asp Asn Phe Lys Arg Leu Asn Phe Thr Gly Phe Ala Lys Ile
266          115          120          125
268 Val Lys Lys His Asp Lys Leu Tyr Pro Lys Tyr Pro Ser Val Lys Ser
269          130          135          140
271 Leu Leu Glu Val Arg Leu Lys Glu Leu Pro Ser His Ser Glu Glu Tyr
272 145          150          155          160
274 Ser Pro Leu Leu Tyr Arg Ile Ser Phe Leu Tyr Asn Ile Leu Arg Ser
275          165          170          175
277 Asn Phe Asn Thr Ala Ser Glu Pro Leu Ala Ser Ala Ser Lys Phe Ser
278          180          185          190
280 Ser Ile Val Ser Asn Asp Ile Asp Met Asn Phe Arg Ser Phe Lys Phe
281          195          200          205
283 Trp Val His Asn Asp Asn Leu Met Glu Val Lys Thr Arg Ile Leu Arg
284          210          215          220
286 His Leu Pro Val Leu Val Tyr Ala Asn Val Pro Ser Glu Asn Asp Asp
287 225          230          235          240
289 Leu Val Asn Arg Phe Glu Ser Asp Ile Ser Asn Asn Asp Glu Ile Val
290          245          250          255
292 Gly Ser Ser Ser Ser Thr Ser Ser Val Glu His Gly Leu Gly Ala Arg
293          260          265          270
295 Ser Phe Asp Pro Leu Ile Asn Thr Leu Tyr Phe Asp Asn Glu His Phe
296          275          280          285
298 Glu Leu Tyr Asn Asp Lys Leu Leu Lys Leu Asn Ser Ala Pro Thr Leu
299          290          295          300
301 Arg Leu Arg Trp Thr Gly Gln Leu Ser Asp Lys Pro Asp Ile Phe Leu
302 305          310          315          320
304 Glu Lys Lys Thr Leu Ile Glu Asp Glu Ala Thr Gly Lys Ser Glu Phe
305          325          330          335
307 Asp Leu Thr Lys Leu Gln Leu Lys Gln Lys Phe Ile Asn Gly Phe Ile
308          340          345          350
310 Phe Glu Gly Asp Lys Lys Phe Lys Glu Gln Thr Leu Lys Lys Leu Lys
311          355          360          365
313 Glu Ser Gly Thr Ala Gly Arg Asp Leu Glu Arg Leu Glu Glu Asp Phe
314          370          375          380
316 Ser Glu Ile Gln Asn Phe Ile Ile Lys Asn Glu Leu Gln Pro Val Phe
317 385          390          395          400
319 Arg Thr Val Tyr Thr Arg Thr Ala Phe Gln Ile Pro Gly Asp Asp Lys
320          405          410          415
322 Ile Arg Val Thr Ile Asp Ser Asn Ile Val Phe Ile Lys Glu Asp Ser
323          420          425          430
325 Phe Asp Arg Glu Arg Pro Ile Arg Asp Pro Asn Thr Trp His Arg Thr
326          435          440          445
328 Asp Ile Asp Ala Asn Val Ala Asn Pro Leu Lys Phe Leu Arg Gly Gly
329          450          455          460
331 Glu Tyr Ala Lys Phe Pro Tyr Ser Val Met Glu Ile Lys Val Lys Ser
332 465          470          475          480
334 Ser Leu Asp Ser Ser Met Ser Ala Ser Ser Met Ile Ser Asn Val Lys

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L:9 M:270 C: Current Application Number differs, Replaced Application Number

L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date